

05-90  
0528 #8

# ENTERED



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## RAW SEQUENCE LISTING

DATE: 06/03/2002

PATENT APPLICATION: US/09/981,087A

TIME: 12:59:23

Input Set : A:\-9-4.app

Output Set: N:\CRF3\06032002\I981087A.raw

3 <110> APPLICANT: Yanofsky, Martin F.  
 4 Liljegren, Sarah  
 5 Farrandiz, Cristina  
 6 The Regents of the University of California  
 8 <120> TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic  
 9 Plants  
 11 <130> FILE REFERENCE: 19452A-000940US  
 13 <140> CURRENT APPLICATION NUMBER: US 09/981,087A  
 C--> 14 <141> CURRENT FILING DATE: 2002-05-21  
 16 <150> PRIOR APPLICATION NUMBER: US 60/090,649  
 17 <151> PRIOR FILING DATE: 1998-06-25  
 19 <150> PRIOR APPLICATION NUMBER: US 09/339,998  
 20 <151> PRIOR FILING DATE: 1999-06-25  
 22 <160> NUMBER OF SEQ ID NOS: 25  
 24 <170> SOFTWARE: PatentIn Ver. 2.1  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 1062  
 28 <212> TYPE: DNA  
 29 <213> ORGANISM: Arabidopsis sp.  
 31 <220> FEATURE:  
 32 <221> NAME/KEY: CDS  
 33 <222> LOCATION: (101)..(829)  
 34 <223> OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)  
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 39 tttctctctc ttgttcttga gattttgaag agagagagat atg gga aga ggt agg 115  
 40 Met Gly Arg Gly Arg  
 41 1 5  
 43 gtt cag ctg aag agg ata gag aac aag atc aat agg caa gtt act ttc 163  
 44 Val Gln Leu Lys Arg Ile Glu Asn Lys Ile Asn Arg Gln Val Thr Phe  
 45 10 15 20  
 47 tca aag aga agg tct ggt ttg ctc aag aaa gct cat gag atc tct gtt 211  
 48 Ser Lys Arg Arg Ser Gly Leu Leu Lys Lys Ala His Glu Ile Ser Val  
 49 25 30 35  
 51 ctc tgc gat gct gag gtt gct ctc atc gtc ttc tct tcc aaa ggc aaa 259  
 52 Leu Cys Asp Ala Glu Val Ala Leu Ile Val Phe Ser Ser Lys Gly Lys  
 53 40 45 50  
 55 ctc ttc gaa tat tcc acc gac tct tgc atg gag agg ata ctt gaa cgc 307  
 56 Leu Phe Glu Tyr Ser Thr Asp Ser Cys Met Glu Arg Ile Leu Glu Arg  
 57 55 60 65  
 59 tat gat cgc tat tta tat tca gac aaa caa ctt gtt ggc cga gac gtt 355  
 60 Tyr Asp Arg Tyr Leu Tyr Ser Asp Lys Gln Leu Val Gly Arg Asp Val  
 61 70 75 80 85

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63 tca caa agt gaa aat tgg gtt cta gaa cat gct aag ctc aag gca aga 403
64 Ser Gln Ser Glu Asn Trp Val Leu Glu His Ala Lys Leu Lys Ala Arg
65          90          95          100
67 gtt gag gta ctt gag aag aac aaa agg aat ttt atg ggg gaa gat ctt 451
68 Val Glu Val Leu Glu Lys Asn Lys Arg Asn Phe Met Gly Glu Asp Leu
69          105          110          115
71 gat tcg ttg agc ttg aag gag ctc caa agc ttg gag cat cag ctc gat 499
72 Asp Ser Leu Ser Leu Lys Glu Leu Gln Ser Leu Glu His Gln Leu Asp
73          120          125          130
75 gca gct atc aag agc att agg tca aga aag aac caa gct atg ttc gaa 547
76 Ala Ala Ile Lys Ser Ile Arg Ser Arg Lys Asn Gln Ala Met Phe Glu
77          135          140          145
79 tcc ata tct gcg ctc cag aag aag gat aaa gcc ttg caa gat cac aac 595
80 Ser Ile Ser Ala Leu Gln Lys Lys Asp Lys Ala Leu Gln Asp His Asn
81 150          155          160          165
83 aat tcg ctt ctc aaa aag att aag gag agg gag aag aaa acg ggt cag 643
84 Asn Ser Leu Leu Lys Lys Ile Lys Glu Arg Glu Lys Lys Thr Gly Gln
85          170          175          180
87 caa gaa gga caa tta gtc caa tgc tcc aac tct tct tca gtt ctt ctg 691
88 Gln Glu Gly Gln Leu Val Gln Cys Ser Asn Ser Ser Ser Val Leu Leu
89          185          190          195
91 cct caa tac tgc gta acc tcc tcc aga gat ggc ttt gtg gag aga gtt 739
92 Pro Gln Tyr Cys Val Thr Ser Ser Arg Asp Gly Phe Val Glu Arg Val
93          200          205          210
95 ggg gga gag aac ggt ggt gca tcg tcg ttg acg gaa cca aac tct ctg 787
96 Gly Gly Glu Asn Gly Gly Ala Ser Ser Leu Thr Glu Pro Asn Ser Leu
97          215          220          225
99 ctt ccg gct tgg atg tta cgt cct acc act acg aac gag tag 829
100 Leu Pro Ala Trp Met Leu Arg Pro Thr Thr Thr Asn Glu
101 230          235          240
103 aactatctca ctctttataa tataatgata atataattaa tgtttaatat tttcataaca 889
105 ttcagcattt ttttggtgac ttataactcat tattaatacc gatatgtttt agctagtcac 949
107 attatatgta tgatggaact ccgttgtcga gacgtatgta cgtaagctat cattagattc 1009
109 actgcgtctt aagaacaaag attcatatct tggtaatgat ttctcatgaa ata 1062
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113 <211> LENGTH: 242
114 <212> TYPE: PRT
115 <213> ORGANISM: Arabidopsis sp.
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120 Arg Gln Val Thr Phe Ser Lys Arg Arg Ser Gly Leu Leu Lys Lys Ala
121 20 25 30
122 His Glu Ile Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Val Phe
123 35 40 45
124 Ser Ser Lys Gly Lys Leu Phe Glu Tyr Ser Thr Asp Ser Cys Met Glu
125 50 55 60
126 Arg Ile Leu Glu Arg Tyr Asp Arg Tyr Leu Tyr Ser Asp Lys Gln Leu
127 65 70 75 80

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128 Val Gly Arg Asp Val Ser Gln Ser Glu Asn Trp Val Leu Glu His Ala
129                      85                      90                      95
130 Lys Leu Lys Ala Arg Val Glu Val Leu Glu Lys Asn Lys Arg Asn Phe
131                      100                      105                      110
132 Met Gly Glu Asp Leu Asp Ser Leu Ser Leu Lys Glu Leu Gln Ser Leu
133                      115                      120                      125
134 Glu His Gln Leu Asp Ala Ala Ile Lys Ser Ile Arg Ser Arg Lys Asn
135                      130                      135                      140
136 Gln Ala Met Phe Glu Ser Ile Ser Ala Leu Gln Lys Lys Asp Lys Ala
137 145                      150                      155                      160
138 Leu Gln Asp His Asn Asn Ser Leu Leu Lys Lys Ile Lys Glu Arg Glu
139                      165                      170                      175
140 Lys Lys Thr Gly Gln Gln Glu Gly Gln Leu Val Gln Cys Ser Asn Ser
141                      180                      185                      190
142 Ser Ser Val Leu Leu Pro Gln Tyr Cys Val Thr Ser Ser Arg Asp Gly
143                      195                      200                      205
144 Phe Val Glu Arg Val Gly Gly Glu Asn Gly Gly Ala Ser Ser Leu Thr
145                      210                      215                      220
146 Glu Pro Asn Ser Leu Leu Pro Ala Trp Met Leu Arg Pro Thr Thr Thr
147 225                      230                      235                      240
148 Asn Glu
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152 <211> LENGTH: 896
153 <212> TYPE: DNA
154 <213> ORGANISM: Arabidopsis sp.
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157 <221> NAME/KEY: CDS
158 <222> LOCATION: (7)..(753)
159 <223> OTHER INFORMATION: AGAMOUS-LIKE 1 (AGL1)
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163      Met Glu Glu Gly Gly Ser Ser His Asp Ala Glu Ser Ser Lys
164      1          5          10
166 aaa cta ggg aga ggg aaa ata gag ata aag agg ata gag aac aca aca      96
167 Lys Leu Gly Arg Gly Lys Ile Glu Ile Lys Arg Ile Glu Asn Thr Thr
168 15          20          25          30
170 aat cgt caa gtt act ttc tgc aaa cga cgc aat ggt ctt ctc aag aaa      144
171 Asn Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu Leu Lys Lys
172          35          40          45
174 gct tat gaa ctc tct gtc ttg tgt gat gcc gaa gtt gcc ctc gtc atc      192
175 Ala Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Val Ile
176          50          55          60
178 ttc tcc act cgt ggc cgt ctc tat gag tac gcc aac aac agt gtg agg      240
179 Phe Ser Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn Ser Val Arg
180          65          70          75
182 ggt aca att gaa agg tac aag aaa gct tgt tcc gat gcc gtc aac cct      288
183 Gly Thr Ile Glu Arg Tyr Lys Lys Ala Cys Ser Asp Ala Val Asn Pro
184          80          85          90
186 cct tcc gtc acc gaa gct aat act cag tac tat cag caa gaa gcc tct      336

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188 95 100 105 110
190 aag ctt cgg agg cag att cga gat att cag aat tca aat agg cat att 384
191 Lys Leu Arg Arg Gln Ile Arg Asp Ile Gln Asn Ser Asn Arg His Ile
192 115 120 125
194 gtt ggg gaa tca ctt ggt tcc ttg aac ttc aag gaa ctc aaa aac cta 432
195 Val Gly Glu Ser Leu Gly Ser Leu Asn Phe Lys Glu Leu Lys Asn Leu
196 130 135 140
198 gaa gga cgt ctt gaa aaa gga atc agc cgt gtc cgc tcc aaa aag aat 480
199 Glu Gly Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser Lys Lys Asn
200 145 150 155
202 gag ctg tta gtg gca gag ata gag tat atg cag aag agg gaa atg gag 528
203 Glu Leu Leu Val Ala Glu Ile Glu Tyr Met Gln Lys Arg Glu Met Glu
204 160 165 170
206 ttg caa cac aat aac atg tac ctg cga gca aag ata gcc gaa ggc gcc 576
207 Leu Gln His Asn Asn Met Tyr Leu Arg Ala Lys Ile Ala Glu Gly Ala
208 175 180 185 190
210 aga ttg aat ccg gac cag cag gaa tcg agt gtg ata caa ggg acg aca 624
211 Arg Leu Asn Pro Asp Gln Gln Glu Ser Ser Val Ile Gln Gly Thr Thr
212 195 200 205
214 gtt tac gaa tcc ggt gta tct tct cat gac cag tcg cag cat tat aat 672
215 Val Tyr Glu Ser Gly Val Ser Ser His Asp Gln Ser Gln His Tyr Asn
216 210 215 220
218 cgg aac tat att ccg gtg aac ctt ctt gaa ccg aat cag caa ttc tcc 720
219 Arg Asn Tyr Ile Pro Val Asn Leu Leu Glu Pro Asn Gln Gln Phe Ser
220 225 230 235
222 ggc caa gac caa cct cct ctt caa ctt gtg taa ctcaaaacat gataacttgt 773
223 Gly Gln Asp Gln Pro Pro Leu Gln Leu Val
224 240 245
226 ttcttccct cataacgatt aagagagaga cgagagagtt cattttatat ttataacgcg 833
228 actgtgtatt catagtttag gttctaataa tgataataac aaaactgttg tttctttgct 893
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234 <211> LENGTH: 248
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242 20 25 30
243 Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala Tyr
244 35 40 45
245 Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Val Ile Phe Ser
246 50 55 60
247 Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn Ser Val Arg Gly Thr
248 65 70 75 80
249 Ile Glu Arg Tyr Lys Lys Ala Cys Ser Asp Ala Val Asn Pro Pro Ser
250 85 90 95

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251 Val Thr Glu Ala Asn Thr Gln Tyr Tyr Gln Gln Glu Ala Ser Lys Leu
252          100          105          110
253 Arg Arg Gln Ile Arg Asp Ile Gln Asn Ser Asn Arg His Ile Val Gly
254          115          120          125
255 Glu Ser Leu Gly Ser Leu Asn Phe Lys Glu Leu Lys Asn Leu Glu Gly
256          130          135          140
257 Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser Lys Lys Asn Glu Leu
258 145          150          155          160
259 Leu Val Ala Glu Ile Glu Tyr Met Gln Lys Arg Glu Met Glu Leu Gln
260          165          170          175
261 His Asn Asn Met Tyr Leu Arg Ala Lys Ile Ala Glu Gly Ala Arg Leu
262          180          185          190
263 Asn Pro Asp Gln Gln Glu Ser Ser Val Ile Gln Gly Thr Thr Val Tyr
264          195          200          205
265 Glu Ser Gly Val Ser Ser His Asp Gln Ser Gln His Tyr Asn Arg Asn
266          210          215          220
267 Tyr Ile Pro Val Asn Leu Leu Glu Pro Asn Gln Gln Phe Ser Gly Gln
268 225          230          235          240
269 Asp Gln Pro Pro Leu Gln Leu Val
270          245
273 <210> SEQ ID NO: 5
274 <211> LENGTH: 959
275 <212> TYPE: DNA
276 <213> ORGANISM: Arabidopsis sp.
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279 <221> NAME/KEY: CDS
280 <222> LOCATION: (78)..(818)
281 <223> OTHER INFORMATION: AGAMOUS-LIKE 5 (AGL5)
283 <400> SEQUENCE: 5
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286 agctagggct tatagaa atg gag ggt ggt gcg agt aat gaa gta gca gag 110
287          Met Glu Gly Gly Ala Ser Asn Glu Val Ala Glu
288          1          5          10
290 agc agc aag aag ata ggg aga ggg aag ata gag ata aag agg ata gag 158
291 Ser Ser Lys Lys Ile Gly Arg Gly Lys Ile Glu Ile Lys Arg Ile Glu
292          15          20          25
294 aac act acg aat cgt caa gtc act ttc tgc aaa cga cgc aat ggt tta 206
295 Asn Thr Thr Asn Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu
296          30          35          40
298 ctc aag aaa gct tat gag ctc tct gtc ttg tgt gac gct gag gtt gct 254
299 Leu Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala
300          45          50          55
302 ctt gtc atc ttc tcc act cga ggc cgt ctc tac gag tac gcc aac aac 302
303 Leu Val Ile Phe Ser Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn
304 60          65          70          75
306 agt gtg aga gga aca ata gaa agg tac aag aag gct tgc tcc gac gcc 350
307 Ser Val Arg Gly Thr Ile Glu Arg Tyr Lys Lys Ala Cys Ser Asp Ala
308          80          85          90
310 gtt aac cct ccg acc atc acc gaa gct aat act cag tac tat cag caa 398

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/981,087A

DATE: 06/03/2002

TIME: 12:59:24

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L:403 M:283 W: Missing Blank Line separator, <400> field identifier  
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